This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.



For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

Part 1: **TITLE, AUTHORS, etc**

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| **Code assigned:** | ***2017.007D*** | | | | (to be completed by ICTV officers) |
| **Short title:** Create 8 species within the family *Polyomaviridae* | | | | | |
| **Modules attached** | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Sébastien Calvignac-Spencer, Matthew D. Daugherty, Mariet C.W. Feltkamp, Chris Lauber, Ugo Moens, Torbjörn Ramqvist, Ernst J. Verschoor, Bernhard Ehlers | | | | | |
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| Bernhard Ehlers, ehlersb@rki.de | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| Polyomaviridae SG | | |  | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| Date first submitted to ICTV: | | | | 6 June 2017 | |
| Date of this revision (if different to above): | | | | 16 June 2017 | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.007D.N.v1.Polyomaviridae\_sp |

**Part 4:** **APPENDIX**: supporting material

| **References:** |
| --- |
| 1 Dill, J. A., Ng, T. F., & Camus, A. C. (2016). Complete sequence of the smallest polyomavirus genome, giant guitarfish (Rhynchobatus djiddensis) polyomavirus 1. *Genome Announcements*, *4*(3), e00391-16.  2 Buck, C. B., Van Doorslaer, K., Peretti, A., Geoghegan, E. M., Tisza, M. J., An, P., ... & McDermott, A. J. (2016). The ancient evolutionary history of polyomaviruses. *PLoS Pathog*, *12*(4), e1005574.  3 Cruz, F. N. D., Li, L., Delwart, E., & Pesavento, P. A. (2017). A novel pulmonary polyomavirus in alpacas (Vicugna pacos). *Veterinary Microbiology*, *201*, 49-55.  4 Heenemann, K., Sieg, M., Rueckner, A., & Vahlenkamp, T. W. (2015). Complete genome sequence of a novel avian polyomavirus isolated from Gouldian finch. *Genome Announcements*, *3*(5), e01001-15.  5 Rigatti, L. H., Toptan, T., Newsome, J. T., Moore, P. S., & Chang, Y. (2016). Identification and characterization of novel rat polyomavirus 2 in a colony of X-SCID rats by P-PIT assay. *mSphere*, *1*(6), e00334-16.  6 Varsani, A., Frankfurter, G., Stainton, D., Male, M. F., Kraberger, S., & Burns, J. M. (2017). Identification of a polyomavirus in Weddell seal (Leptonychotes weddellii) from the Ross Sea (Antarctica). *Archives of Virology*, *162*(5):1403-1407.  7 Ben Salem, N., Leendertz, F. H., & Ehlers, B. (2016). Genome sequences of polyomaviruses from the wild-living red colobus (Piliocolobus badius) and western chimpanzee (Pan troglodytes verus). *Genome Announcements*, *4*(5), e01101-16.  8 Marton, S., Erdélyi, K., Dán, Á., Bányai, K., & Fehér, E. (2016). Complete genome sequence of a variant Pyrrhula pyrrhula polyomavirus 1 strain isolated from white-headed munia (Lonchura maja). *Genome Announcements*, *4*(6), e01172-16.  9 Calvignac-Spencer, S., Feltkamp, M., Daugherty, M.D., Moens, U., Ramqvist, T., Johne, R., Ehlers, B. (2015). ICTV taxonomic proposal 2015.015a-aaD.A.v2.Polyomaviridae\_rev. In the family *Polyomaviridae*, create 4 genera (*Alphapolyomavirus, Betapolyomavirus, Gammapolyomavirus* and *Deltapolyomavirus*) and reclassify 8 existing species.  <http://www.ictvonline.org/proposals-15/2015.015a-aaD.A.v2.Polyomaviridae_rev.pdf>  10 Calvignac-Spencer, S., et al. (2016) A taxonomy update for the family *Polyomaviridae*. *Archives of Virology* 161(6), 1739-1750. |

**Reasons to justify the creation and assignment of the 8 new species:**

1. Genomes of giant guitarfish polyomavirus (GfPyV1), alpaca polyomavirus (AlPyV), rat polyomavirus 2 (RatPyV2), Weddell seal polyomavirus (WsPyV), Piliocolobus badius polyomavirus 2 (PbadPyV2), Hungarian finch polyomavirus (HfPyV), Erythrura gouldiae (Gouldian finch) polyomavirus 1 (EgouPyV1), sharp-spined notothenia polyomavirus (SspPyV) that are the respective members of the 8 proposed species (Rhynchobatus djiddensis polyomavirus 1, Vicugna pacos polyomavirus 1, Rattus norvegicus polyomavirus 2, Leptonychotes weddellii polyomavirus 1,Piliocolobus badius polyomavirus 1, Lonchura maja polyomavirus 1, Erythrura gouldiae polyomavirus 1, Trematomus pennellii polyomavirus 1) are published (1-8). This fulfills number 1 of the species definition criteria published in 2016 by the Polyomaviridae Study Group and ratified by ICTV in May 2016 (9, 10).
2. GfPyV1, AlPyV, RatPyV2, WsPyV, PbadPyV2, HfPyV, EgouPyV1 have a genome organization typical for members of the *Polyomaviridae*. This fulfills number 2 of the species definition criteria.  
   SspPyV encodes LTAg, VP1, and VP2 and therefore has a genome organization resembling that of mammalian members of the *Polyomaviridae* (except that an STAg CDS is missing). This fulfills number 2 of the species definition criteria.
3. **GfPyV1**: there is sufficient information that GfPyV1 is naturally hosted by member of the host species *Rhynchobatus djiddensis*: GfPyV1 was identified in skin lesions of giant guitarfish, and 1 full genome is available (deposited in GenBank under the accession number KP264963). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of GfPyV1 was compared pairwise with those of other PyVs. GfPyV1 LTAg CDS and LTAg CDS of black sea bass polyomavirus (BassPyV, acc.no. KP071318; species *Centropristis striata polyomavirus 1*) were most closely related (72 % observed genetic distance). This fulfills number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS).  
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, GfPyV1 displays a unique position at the basis of the tree (Fig. 1).
4. **AlPyV**: There is sufficient information that AlPyV is naturally hosted by members of the host species *Vicugna pacos*: AlPyV was identified in lungs of 7 alpacas (Cruz et al., 2017). A full genome is available (deposited in GenBank under the accession number KU879245). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of AlPyV was compared pairwise with those of other PyVs. AlPyV LTAg CDS and LTAg CDS of KI polyomavirus (species *Human polyomavirus 3*) were most closely related (40 % observed genetic distance). This fulfills number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS).   
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, AlPyV clusters with members of the genus *Betapolyomavirus* (Fig, 1).
5. **RatPyV2**: There is sufficient information that RatPyV2 is naturally hosted by member of the host species *Rattus norvegicus*: RatPyV2 was identified in diverse organs of laboratory rats (Rigatti et al., 2016). A full genome is available (deposited in GenBank under the accession number KX574453). This fulfills number 3 of the species definition criteria.  
   In addition, a RatPyV2 genome (isolate 1014-2016-2) that is 99% identical to RatPyV2 genome and displays an identical LTAg CDS, was identified in immunodeficient laboratory rats and deposited in GenBank by Besch-Williford et al. (acc.no. KX808699).  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of RatPyV2 was compared pairwise with those of other PyVs. RatPyV2 LTAg CDS and LTAg CDS of bank vole polyomavirus (acc.no. KR612368; species *Myodes glareolus* *polyomavirus 1*) were most closely related (39 % observed genetic distance). This fulfills number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS).

In phylogenetic analysis with LTAg CDS of published polyomaviruses, RatPyV2 clusters with bank vole polyomavirus and other members of the genus *Betapolyomavirus* (Fig. 1).

1. **WsPyV** (Weddell seal polyomavirus): there is sufficient information that WsPyV is naturally hosted by member of the host species *Leptonychotes weddellii*: WsPyV was identified in an organ (kidney) and not in a metagenomic sample (as e.g. stool). One full genome is available (deposited in GenBank under the accession number KX533457). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of WsPyV was compared pairwise with those of other PyVs. WsPyV LTAg CDS and LTAg CDS of California sea lion polyomavirus (CslPyV; species *Zalophus californianus* *polyomavirus 1*) were most closely related (15 % observed genetic distance). This fulfills almost completely number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS). As WsPyV and CslPyV were identified in two different seal species (see number 5 of the species definition criteria) and mammalian polyomaviruses have so far not been reported to infect foreign hosts, the creation of the species *Leptonychotes weddellii polyomavirus 1* is justified.  
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, WsPyV clusters with CslPyV and other members of the genus *Betapolyomavirus* (Fig. 1).
2. **PbadPyV2**: there is sufficient information that PbadPyV2 is naturally hosted by Tana River red colobus, member of the species *Piliocolobus badius*: Lymphoid organs (spleen, lymph node) of 4 wild-living individuals from Ivory coast were PCR-positive (sequence confirmed). One full genome is available (deposited in GenBank under the accession number KX509984). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of PbadPyV2 was compared pairwise with those of other PyVs. PbadPyV2 LTAg CDS and LTAg CDS of Piliocolobus rufomitratus polyomavirus 1 (species *Piliocolobus rufomitratus* *polyomavirus 1*) were most closely related (8 % observed genetic distance). This does not fulfill number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS). However, number five can override number 4 of the species definition criteria: “ When two polyomaviruses exhibit <15 % observed genetic distance, biological properties (e.g., host specificity, disease association, tissue tropism, etc.) can justify the creation of a new species.“ As *Piliocolobus badius* and *Piliocolobus rufomitratus* are 2 distinct host species and mammalian polyomaviruses have so far not been reported to infect foreign hosts, the creation of the species *Piliocolobus badius* *polyomavirus 1* is justified.  
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, PbadPyV2 clusters with Piliocolobus rufomitratus polyomavirus 1 and other members of the genus *Alphapolyomavirus* (Fig. 1).
3. **HfPyV**: there is sufficient information that HfPyV is naturally hosted by members of the host species *Lonchura maja*: HfPyV was identified in pooled lungs and livers of a flock of Hungarian finches (Marton et al., 2016). A full genome is available (deposited in GenBank under the accession number KX756154). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of HfPyV was compared pairwise with those of other PyVs. HfPyV LTAg CDS and LTAg CDS of finch polyomavirus from Eurasian bullfinch (acc.no. DQ192571; species *Pyrrhula pyrrhula polyomavirus 1*) were most closely related (8.5% observed genetic distance). This does not fulfill number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS). However, number five can override number 4 of the species definition criteria: “ When two polyomaviruses exhibit <15 % observed genetic distance, biological properties (e.g., host specificity, disease association, tissue tropism, etc.) can justify the creation of a new species.“ As *Lonchura maja* and *Pyrrhula pyrrhula* are 2 distinct host species, the creation of the species *Lonchura maja polyomavirus 1* is justified.  
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, HfPyV clusters with finch polyomavirus (acc.no. DQ192571) and other members of the genus *Gammapolyomavirus* (Fig. 1).
4. **EgouPyV1**: there is sufficient information that EgouPyV1 is naturally hosted by member of the host species *Erythrura gouldiae*: EgouPyV1was identified in liver of a Gouldian finch (Heenemann et al., 2016). A full genome is available (deposited in GenBank under the accession number KX756154). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of EgouPyV1was compared pairwise with those of other PyVs. EgouPyV1 LTAg CDS and LTAg CDS of crow polyomavirus from Eurasian jackdaw (acc.no. DQ192570; species *Corvus monedula polyomavirus 1*) were most closely related (23% observed genetic distance). This fulfills number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS).   
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, EgouPyV1 clusters with crow polyomavirus (acc.no. DQ192571) and other members of the genus *Gammapolyomavirus* (Fig. 1).
5. **SspPyV**: there is sufficient information that sharp-spined notothenia polyomavirus (SspPyV) is naturally hosted by member of the host species *Trematomus pennellii*: SspPyV was identified in pooled organs of 7 notothenia individuals. A full genome is available (deposited in GenBank under the accession number KP768176). This fulfills number 3 of the species definition criteria.  
   Using the MAFFT module in Geneious 10.0.5., the LTAg CDS of SspPyV was compared pairwise with those of other PyVs. SspPyV LTAg CDS and LTAg CDS of black sea bass polyomavirus (BassPyV, acc.no. KP071318; species *Centropristis striata polyomavirus 1*) were most closely related (57 % observed genetic distance). This fulfills number 4 of the species definition criteria (>15 % observed genetic distance on basis of LTAg CDS).  
   In phylogenetic analysis with LTAg CDS of published polyomaviruses, SspPyV clusters with BassPyV (Fig. 1).

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**Figure 1**. Maximum likelihood tree based on an alignment of large T sequences (503 amino acid positions) reconstructed with PhyML v3.1. Model of aa substitution (determined with ProtTest v3.2): LG+I+G+F. Branch support values: Shimodaira-Hasegawa-like approximate likelihood ratio tests (SH-like aLRT), grey branches: <0.95 SH-like aLRT. Proposed novel species are in enlarged, black font.

